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Sequence Listing could not be accepted due to errors.  
See attached Validation Report.  
If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).  
Reviewer: markspencer  
Timestamp: Mon May 07 13:37:20 EDT 2007  
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\*\*\*\*\*

Reviewer Comments:

ErrorCode	ErrorDescription
W213	Artificial or Unknown found in <213> in SEQ ID (6)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
Feature <220> and <223> required explaining the source of the genetic material when "Artificial" or "Unknown" are used as the organism.	
W213	Artificial or Unknown found in <213> in SEQ ID (7)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
Same as above.	
W213	Artificial or Unknown found in <213> in SEQ ID (12)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
Same as above	
W213	Artificial or Unknown found in <213> in SEQ ID (13)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
Same as above	
W213	Artificial or Unknown found in <213> in SEQ ID (19)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
Same as above	
W213	Artificial or Unknown found in <213> in SEQ ID (20)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
Same as above	
W213	Artificial or Unknown found in <213> in SEQ ID (25)
E224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (25)

Same as above

W213 Artificial or Unknown found in <213> in SEQ ID (26)

E224 <220>,<223> section required as <213> has Artificial  
sequence or Unknown in SEQID (26)

Same as above

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(155)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(160)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(165)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(170)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(175)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(180)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(185)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(190)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(195)

E323 Invalid/missing amino acid numbering SEQID (11) POS  
(200)

Nubering for SEQ ID # 11 is missing number 155 and number 205 is used  
twice.

\*\*\*\*\*

Application No: 10583785

Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2007-05-07 12:52:44.341  
**Finished:** 2007-05-07 12:52:49.535  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 194 ms  
**Total Warnings:** 8  
**Total Errors:** 18  
**No. of SeqIDs Defined:** 26  
**Actual SeqID Count:** 26

<b>ErrCode</b>	<b>Error Description</b>
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (155)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (160)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (165)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (170)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (175)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (180)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (185)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (190)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (195)
E 323	Invalid/missing amino acid numbering SEQID (11) POS (200)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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**Input Set:**

**Output Set:**

**Started:** 2007-05-07 12:52:44.341  
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<b>ErrCode</b>	<b>Error Description</b>
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
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W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (26)

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger

<120> Novel chimeric plasminogen activators and their pharmaceutical use

<130> 607927-000001

<140> 10583785

<141> 2007-05-07

<150> US/10/583,785

<151> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

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atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg	864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275 280 285	
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290 295 300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala	
305 310 315 320	
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag	1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys	
325 330 335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg	1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg	
340 345 350	

ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc 1104  
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr  
355 360 365

atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt 1143  
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu  
370 375 380

<210> 2

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<400> 2

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1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240  
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288  
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336  
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384  
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa 432  
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
130 135 140

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg 480  
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
145 150 155 160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc 528  
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
165 170 175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac 576  
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
180 185 190

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc 624  
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
195 200 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag 672  
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
210 215 220

ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg 720  
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
225 230 235 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc 768  
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
245 250 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc 816  
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg  
260 265 270

ctc gtc ctc cgg tgc tcc atg 837  
Leu Val Leu Arg Cys Ser Met  
275

<210> 3  
<211> 237  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) ... (237)  
<223> Coding sequence of the mature surfactant protein B

<400> 3

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Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys  
1 5 10 15

cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc 96  
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala  
20 25 30

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc 144  
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys  
35 40 45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc 192  
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg  
50 55 60

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg 237  
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met  
65 70 75

<210> 4

<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

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1 5 10 15

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac 96  
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
20 25 30

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144  
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
35 40 45

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192  
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
50 55 60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240  
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
65 70 75 80

aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct 288  
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
85 90 95

gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt 336  
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
100 105 110

cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg 384  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
115 120 125

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	
gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val	
195 200 205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac	672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His	
210 215 220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt	720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly	
225 230 235 240	
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg	768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val	
245 250 255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac	816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His	
260 265 270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt	864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys	
275 280 285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat	912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr	
290 295 300	
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa	960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys	
305 310 315 320	
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt	1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val	
325 330 335	
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc	1056
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly	
340 345 350	
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa	1104

Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys
355					360					365					

aca	gat	tcc	tgc	cag	gga	gac	tca	ggg	gga	ccc	ctc	gtc	tgt	tcc	ctc	1152
Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	
370				375				380								

caa	ggc	cgc	atg	act	ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	1200
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	
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Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	
405					410					415						

ccc	tgg	atc	cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc	1293
Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	
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<210> 5

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (828)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 5

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Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	
1				5				10				15				

act	ctg	agg	ccc	cgc	ttt	aag	att	att	ggg	gga	gaa	ttc	acc	acc	atc	96		
Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile			
				20						25						30		

gag	aac	cag	ccc	tgg	ttt	gcg	gcc	atc	tac	agg	agg	cac	cgg	ggg	ggc	144
Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	
35				40				45								

tct	gtc	acc	tac	gtg	tgt	gga	ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	192
Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	
50			55			60										

atc	agc	gcc	aca	cac	tgc	ttc	att	gat	tac	cca	aag	aag	gag	gac	tac	240
Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	
65		70				75				80						

atc	gtc	tac	ctg	ggt	cgc	tca	agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	288
Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	
				85		90				95						

atg	aag	ttt	gag	gtg	gaa	aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	336
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Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	
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Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	
		115						120				125				
aag	gag	ggc	agg	tgt	gcg	cag	cca	tcc	cgg	act	ata	cag	acc	atc	tgc	432
Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	
		130				135					140					
ctg	ccc	tcg	atg	tat	aac	gat	ccc	cag	ttt	ggc	aca	agc	tgt	gag	atc	480
Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	
145					150				155					160		
act	ggc	ttt	gga	aaa	gag	aat	tct	acc	gac	tat	ctc	tat	ccg	gag	cag	528
Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	
			165					170					175			
ctg	aaa	atg	act	gtt	gtg	aag	ctg	att	tcc	cac	cgg	gag	tgt	cag	cag	576
Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	
			180					185					190			